



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2026 – 03:14 PM UTC

PDB ID : 5L0Q / pdb_00005l0q
Title : Crystal structure of the complex between ADAM10 D+C domain and a conformation specific mAb 8C7.
Authors : Xu, K.; Saha, N.; Nikolov, D.B.
Deposited on : 2016-07-28
Resolution : 2.76 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

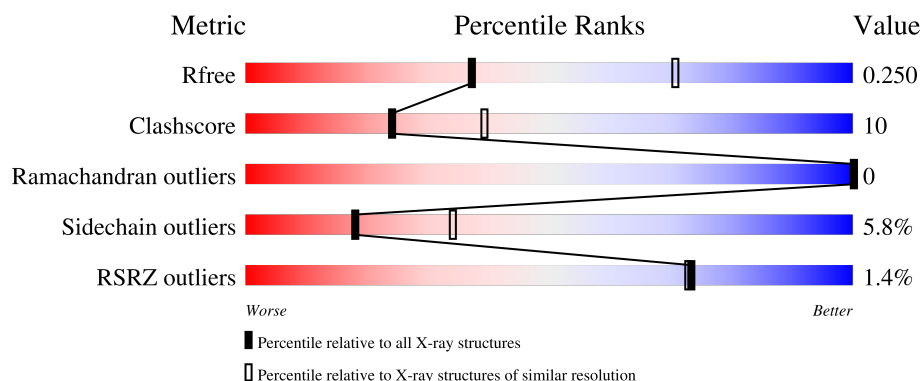
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.76 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1009 (2.76-2.76)
Clashscore	190562	1044 (2.76-2.76)
Ramachandran outliers	187476	1024 (2.76-2.76)
Sidechain outliers	187428	1024 (2.76-2.76)
RSRZ outliers	180081	1009 (2.76-2.76)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	203	5% 65% 31% .
1	D	203	% 71% 23% ..
2	B	214	79% 19% ..
2	E	214	75% 20% ..
3	C	222	% 82% 14% .

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Mol	Chain	Length	Quality of chain
3	F	222	% 78% 17% ..

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	SO4	A	703	-	-	X	-
5	SO4	D	703	-	-	X	-

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 9942 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Disintegrin and metalloproteinase domain-containing protein 10.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	203	Total	C	N	O	S	0	0	0
			1493	893	265	303	32			
1	D	195	Total	C	N	O	S	0	0	0
			1440	860	256	292	32			

There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	450	PRO	-	expression tag	UNP Q10741
A	451	VAL	-	expression tag	UNP Q10741
A	452	GLY	-	expression tag	UNP Q10741
A	453	LEU	-	expression tag	UNP Q10741
A	454	ALA	-	expression tag	UNP Q10741
A	647	GLY	-	expression tag	UNP Q10741
A	648	SER	-	expression tag	UNP Q10741
A	649	ALA	-	expression tag	UNP Q10741
A	650	SER	-	expression tag	UNP Q10741
A	651	GLY	-	expression tag	UNP Q10741
A	652	LEU	-	expression tag	UNP Q10741
D	450	PRO	-	expression tag	UNP Q10741
D	451	VAL	-	expression tag	UNP Q10741
D	452	GLY	-	expression tag	UNP Q10741
D	453	LEU	-	expression tag	UNP Q10741
D	454	ALA	-	expression tag	UNP Q10741
D	647	GLY	-	expression tag	UNP Q10741
D	648	SER	-	expression tag	UNP Q10741
D	649	ALA	-	expression tag	UNP Q10741
D	650	SER	-	expression tag	UNP Q10741
D	651	GLY	-	expression tag	UNP Q10741
D	652	LEU	-	expression tag	UNP Q10741

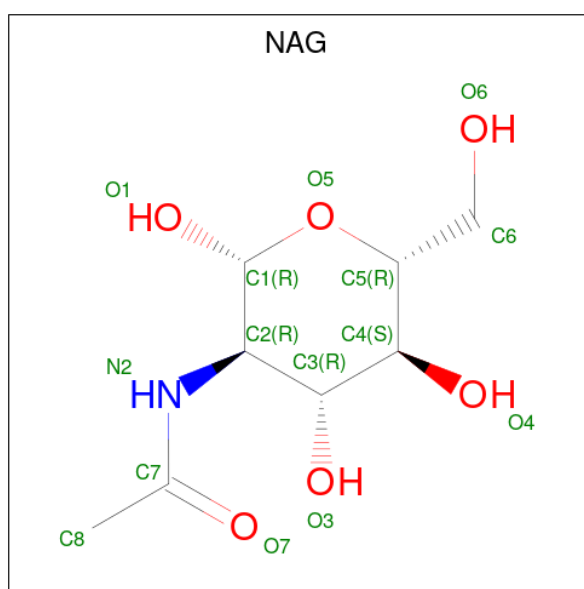
- Molecule 2 is a protein called mAb 8C7 light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	212	Total	C	N	O	S	0	0	0
			1645	1024	281	334	6			
2	E	212	Total	C	N	O	S	0	0	0
			1651	1027	284	334	6			

- Molecule 3 is a protein called mAb 8C7 heavy chain.

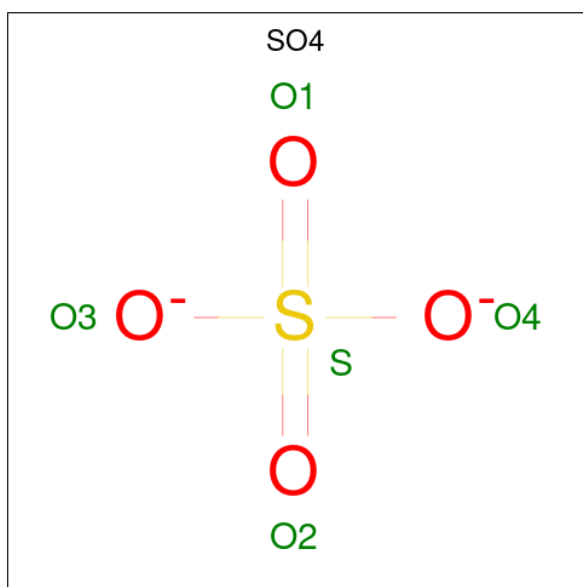
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	213	Total	C	N	O	S	0	0	0
			1624	1031	268	318	7			
3	F	214	Total	C	N	O	S	0	0	0
			1632	1035	269	321	7			

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			14	8	1	5		
4	C	1	Total	C	N	O	0	0
			14	8	1	5		
4	D	1	Total	C	N	O	0	0
			14	8	1	5		
4	F	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 5 is SULFATE ION (CCD ID: SO4) (formula: O_4S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	O	S	0	0
			5	4	1		
5	A	1	Total	O	S	0	0
			5	4	1		
5	A	1	Total	O	S	0	0
			5	4	1		
5	B	1	Total	O	S	0	0
			5	4	1		
5	B	1	Total	O	S	0	0
			5	4	1		
5	C	1	Total	O	S	0	0
			5	4	1		
5	C	1	Total	O	S	0	0
			5	4	1		
5	C	1	Total	O	S	0	0
			5	4	1		
5	D	1	Total	O	S	0	0
			5	4	1		
5	D	1	Total	O	S	0	0
			5	4	1		
5	E	1	Total	O	S	0	0
			5	4	1		
5	E	1	Total	O	S	0	0
			5	4	1		
5	F	1	Total	O	S	0	0
			5	4	1		

- Molecule 6 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	1	Total 1	Mg 1	0	0
6	D	1	Total 1	Mg 1	0	0

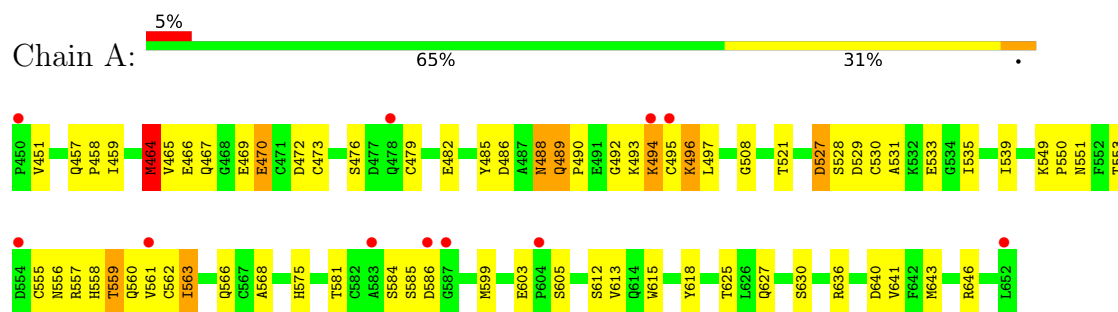
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	40	Total 40	O 40	0	0
7	B	51	Total 51	O 51	0	0
7	C	66	Total 66	O 66	0	0
7	D	44	Total 44	O 44	0	0
7	E	56	Total 56	O 56	0	0
7	F	77	Total 77	O 77	0	0

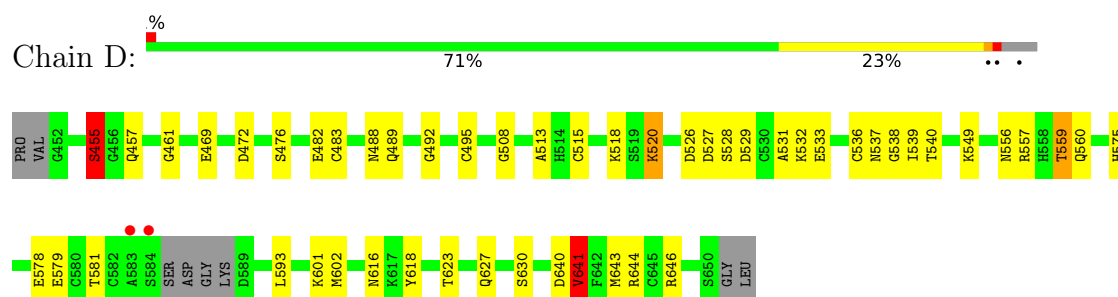
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

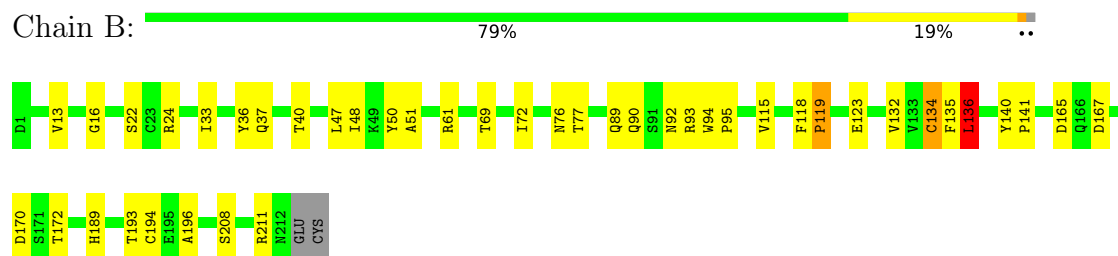
- Molecule 1: Disintegrin and metalloproteinase domain-containing protein 10



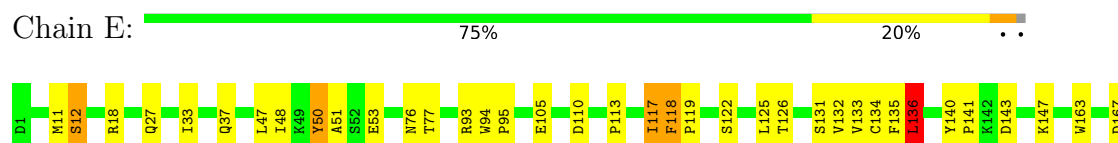
- Molecule 1: Disintegrin and metalloproteinase domain-containing protein 10

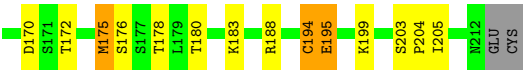


- Molecule 2: mAb 8C7 light chain

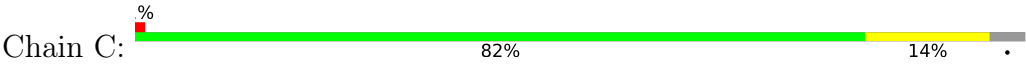


- Molecule 2: mAb 8C7 light chain

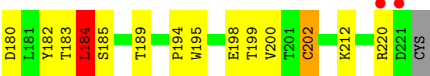
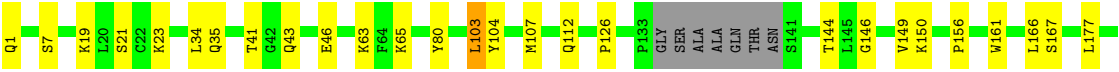
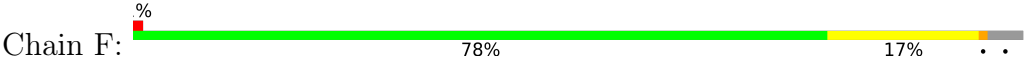




• Molecule 3: mAb 8C7 heavy chain



• Molecule 3: mAb 8C7 heavy chain



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	53.33Å 141.68Å 268.08Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	125.26 – 2.76 125.26 – 2.76	Depositor EDS
% Data completeness (in resolution range)	98.5 (125.26-2.76) 98.6 (125.26-2.76)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.12	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.39 (at 2.77Å)	Xtriage
Refinement program	PHENIX 1.8.2_1309	Depositor
R, R_{free}	0.203 , 0.251 0.207 , 0.250	Depositor DCC
R_{free} test set	2690 reflections (5.09%)	wwPDB-VP
Wilson B-factor (Å ²)	42.3	Xtriage
Anisotropy	0.992	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 43.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	9942	wwPDB-VP
Average B, all atoms (Å ²)	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 20.23 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 9.1058e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, SO4, NAG

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	1.07	9/1519 (0.6%)	1.17	13/2040 (0.6%)
1	D	0.50	0/1464	0.99	10/1965 (0.5%)
2	B	0.74	2/1683 (0.1%)	0.96	3/2286 (0.1%)
2	E	0.76	1/1689 (0.1%)	0.95	2/2293 (0.1%)
3	C	0.57	0/1668	0.89	0/2278
3	F	0.77	4/1676 (0.2%)	0.89	0/2289
All	All	0.75	16/9699 (0.2%)	0.97	28/13151 (0.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	3
1	D	0	2
2	B	0	1
2	E	0	1
3	C	0	3
3	F	0	5
All	All	0	15

The worst 5 of 16 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	F	149	VAL	C-O	-7.57	1.16	1.24
1	A	494	LYS	CA-C	-7.55	1.43	1.52
2	B	134	CYS	C-O	-6.04	1.16	1.24
2	E	136	LEU	C-O	-6.00	1.17	1.23
1	A	459	ILE	CA-C	-5.62	1.45	1.52

The worst 5 of 28 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	494	LYS	N-CA-C	-11.94	93.41	110.24
1	A	489	GLN	N-CA-C	-7.28	99.80	108.25
1	D	508	GLY	CA-C-N	7.01	126.64	119.56
1	D	508	GLY	C-N-CA	7.01	126.64	119.56
2	E	118	PHE	CA-C-N	6.76	127.34	120.38

There are no chirality outliers.

5 of 15 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	490	PRO	Peptide
1	A	584	SER	Peptide
1	A	585	SER	Peptide
2	B	50	TYR	Peptide
3	C	41	THR	Peptide

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1493	0	1381	56	0
1	D	1440	0	1324	30	0
2	B	1645	0	1564	34	0
2	E	1651	0	1575	34	0
3	C	1624	0	1581	15	0
3	F	1632	0	1585	19	0
4	A	14	0	13	5	0
4	C	14	0	13	1	0
4	D	14	0	13	0	0
4	F	14	0	13	2	0
5	A	15	0	0	4	0
5	B	10	0	0	1	0
5	C	15	0	0	0	0
5	D	10	0	0	2	0
5	E	10	0	0	0	0
5	F	5	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	A	1	0	0	0	0
6	D	1	0	0	0	0
7	A	40	0	0	12	0
7	B	51	0	0	3	0
7	C	66	0	0	3	0
7	D	44	0	0	5	0
7	E	56	0	0	4	0
7	F	77	0	0	6	0
All	All	9942	0	9062	186	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 10.

The worst 5 of 186 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:476:SER:OG	1:A:488:ASN:ND2	1.88	1.06
1:A:470:GLU:OE2	1:A:497:LEU:N	1.88	1.05
2:B:193:THR:OG1	2:B:208:SER:OG	1.73	1.04
2:B:135:PHE:C	2:B:136:LEU:HD23	1.84	1.03
2:E:163:TRP:HE1	2:E:175:MET:HE3	1.27	0.99

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	201/203 (99%)	196 (98%)	5 (2%)	0	100	100
1	D	191/203 (94%)	190 (100%)	1 (0%)	0	100	100
2	B	210/214 (98%)	204 (97%)	6 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	E	210/214 (98%)	206 (98%)	4 (2%)	0	100	100
3	C	209/222 (94%)	200 (96%)	9 (4%)	0	100	100
3	F	210/222 (95%)	203 (97%)	7 (3%)	0	100	100
All	All	1231/1278 (96%)	1199 (97%)	32 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	171/171 (100%)	159 (93%)	12 (7%)	14	26
1	D	165/171 (96%)	154 (93%)	11 (7%)	15	28
2	B	189/192 (98%)	181 (96%)	8 (4%)	26	49
2	E	190/192 (99%)	178 (94%)	12 (6%)	16	30
3	C	181/187 (97%)	171 (94%)	10 (6%)	19	37
3	F	182/187 (97%)	172 (94%)	10 (6%)	19	37
All	All	1078/1100 (98%)	1015 (94%)	63 (6%)	18	34

5 of 63 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	C	200	VAL
3	F	65	LYS
1	D	581	THR
3	F	43	GLN
3	F	184	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
2	E	137	ASN
3	F	171	HIS
1	A	627	GLN
2	B	210	ASN
1	D	556	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 19 ligands modelled in this entry, 2 are monoatomic - leaving 17 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
4	NAG	C	301	3	14,14,15	0.50	0	17,19,21	0.67	0
5	SO4	A	703	-	4,4,4	0.34	0	6,6,6	0.34	0
5	SO4	C	304	-	4,4,4	0.32	0	6,6,6	0.38	0
5	SO4	E	301	-	4,4,4	0.30	0	6,6,6	0.14	0
5	SO4	F	302	-	4,4,4	0.35	0	6,6,6	0.20	0
5	SO4	D	702	-	4,4,4	0.27	0	6,6,6	0.09	0
5	SO4	A	702	-	4,4,4	0.27	0	6,6,6	0.12	0
5	SO4	A	704	-	4,4,4	0.27	0	6,6,6	0.45	0
5	SO4	B	302	-	4,4,4	0.34	0	6,6,6	0.24	0
5	SO4	D	703	-	4,4,4	0.25	0	6,6,6	0.19	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	NAG	D	701	1	14,14,15	0.30	0	17,19,21	0.52	0
5	SO4	E	302	-	4,4,4	0.28	0	6,6,6	0.26	0
5	SO4	C	302	-	4,4,4	0.22	0	6,6,6	0.29	0
4	NAG	A	701	1	14,14,15	0.95	1 (7%)	17,19,21	3.32	5 (29%)
4	NAG	F	301	3	14,14,15	0.33	0	17,19,21	0.90	1 (5%)
5	SO4	B	301	-	4,4,4	0.26	0	6,6,6	0.04	0
5	SO4	C	303	-	4,4,4	0.36	0	6,6,6	0.14	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAG	C	301	3	-	2/6/23/26	0/1/1/1
4	NAG	F	301	3	-	2/6/23/26	0/1/1/1
4	NAG	D	701	1	-	0/6/23/26	0/1/1/1
4	NAG	A	701	1	-	5/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	701	NAG	C2-N2	-2.01	1.42	1.46

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	701	NAG	C1-O5-C5	9.60	125.05	112.19
4	A	701	NAG	C4-C3-C2	-6.24	101.88	111.02
4	A	701	NAG	C2-N2-C7	-4.55	116.81	122.90
4	A	701	NAG	C3-C4-C5	-4.33	102.38	110.23
4	F	301	NAG	C1-O5-C5	2.99	116.19	112.19

There are no chirality outliers.

5 of 9 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	701	NAG	C8-C7-N2-C2
4	A	701	NAG	O7-C7-N2-C2
4	F	301	NAG	O5-C5-C6-O6

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Mol	Chain	Res	Type	Atoms
4	C	301	NAG	O5-C5-C6-O6
4	C	301	NAG	C4-C5-C6-O6

There are no ring outliers.

8 monomers are involved in 15 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	C	301	NAG	1	0
5	A	703	SO4	2	0
5	A	702	SO4	1	0
5	A	704	SO4	1	0
5	D	703	SO4	2	0
4	A	701	NAG	5	0
4	F	301	NAG	2	0
5	B	301	SO4	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	203/203 (100%)	0.32	11 (5%) 31 31	13, 40, 64, 80	0
1	D	195/203 (96%)	0.14	2 (1%) 79 79	13, 40, 58, 79	0
2	B	212/214 (99%)	-0.23	0 100 100	11, 25, 68, 74	0
2	E	212/214 (99%)	-0.23	0 100 100	9, 24, 67, 73	0
3	C	213/222 (95%)	-0.26	2 (0%) 81 81	12, 25, 48, 65	0
3	F	214/222 (96%)	-0.25	2 (0%) 81 81	11, 25, 47, 83	0
All	All	1249/1278 (97%)	-0.09	17 (1%) 73 73	9, 29, 62, 83	0

The worst 5 of 17 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	495	CYS	4.9
1	A	450	PRO	2.8
3	F	220	ARG	2.8
1	A	494	LYS	2.6
1	A	583	ALA	2.6

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	NAG	A	701	14/15	0.70	0.17	66,74,80,81	0
4	NAG	C	301	14/15	0.74	0.12	39,48,58,59	0
4	NAG	D	701	14/15	0.75	0.16	52,60,65,67	0
4	NAG	F	301	14/15	0.78	0.11	42,48,54,57	0
5	SO4	D	702	5/5	0.86	0.16	57,59,64,78	0
5	SO4	B	301	5/5	0.87	0.14	44,54,63,75	0
6	MG	A	705	1/1	0.87	0.25	28,28,28,28	0
5	SO4	A	703	5/5	0.88	0.15	43,44,63,71	0
5	SO4	A	702	5/5	0.89	0.16	45,54,63,65	0
5	SO4	C	302	5/5	0.90	0.14	39,40,47,53	0
5	SO4	E	302	5/5	0.92	0.16	39,39,47,59	0
5	SO4	B	302	5/5	0.93	0.13	39,40,49,66	0
5	SO4	D	703	5/5	0.94	0.10	45,47,56,57	0
5	SO4	F	302	5/5	0.94	0.16	33,34,46,65	0
5	SO4	E	301	5/5	0.94	0.14	37,37,46,53	0
5	SO4	A	704	5/5	0.95	0.11	37,40,44,45	0
5	SO4	C	303	5/5	0.95	0.16	32,34,47,55	0
5	SO4	C	304	5/5	0.98	0.05	21,21,22,26	0
6	MG	D	704	1/1	0.99	0.11	33,33,33,33	0

6.5 Other polymers [i](#)

There are no such residues in this entry.